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CERTIFICATE OF MAILING UNDER 37 C.F.R. §1.8(a)

The undersigned hereby certifies that this document is being placed in the United States mail with first-class postage attached, addressed to MAIL STOP AMENDMENT, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on the 21st day of November, 2006.

Christine M. Colbert
Christine M. Colbert

MAIL STOP AMENDMENT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 C.F.R. § 1.132

1. I, Gerald Fitzgerald, am a microbiologist and Professor of Microbiology at University College Cork, Ireland (UCC). A copy of my Curriculum Vitae is attached as Exhibit 1.

2. I have been Director of the National Food Biotechnology Center (NFBC) at UCC from 1998 to 2004. I am co-author of the paper entitled "Determination of Genetic Diversity Within The Genus *Bifidobacterium* and Estimation of Chromosomal Size," by O'Riordan and Fitzgerald (FEMS Microbiology Letters 156 (1997) 259-264), referred to as the O'Riordan and Fitzgerald paper. This paper is cited in the Information Disclosure Statements filed in the referenced application. A copy of this paper is attached as Exhibit 2.

3. I am one of the founder members of Alimentary Health and a shareholder in Alimentary Health. Alimentary Health is a campus-based specialty biotechnology company founded in 1999 to commercialize output of research from the UCC/BioResearch Ireland (BRI) probiotic research program. UCC is a sharelolder in Alimentary Health. The UCC Probiotic Group and Alimentary Health, as the Group's corporate partner, secured funding from Science Foundation Ireland; the Alimentary Pharmabiotic Centre was formed as a result. My research funding is derived from government grants and industry contracts, the latter primarily with Alimentary Health. My research activities are carried out with UCC, both in APC and Alimentary Health laboratories.

4. I have read the above-identified patent application and the pending claims.

5. The O'Riordan and Fitzgerald paper describes a genetic method to distinguish among different bifidobacterial species. Table 1 of the O'Riordan and Fitzgerald paper lists UCC 35624 as one of the organisms analyzed. It also indicates the source of UCC 35624 is human intestine. UCC35624 is an internal designation given to a strain obtained by researchers in the Department of Microbiology at UCC. One skilled in the art could not have obtained this specific strain using information contained in the O'Riordan and Fitzgerald paper and information available to those in the art at the time the paper was published. The paper is not enabling.

6. Bacterial strain Bifidobacterium infantis 35624 was not available to the public. A sample of the strain was not placed in the NCIMB until 1999. Maintenance and control of the strain was managed by the NFBC, under my Directorship. The public did not have access to the strain; anyone who had an interest in obtaining it would have had to make a request to the NFBC, and agree to comply with terms of a strict material transfer agreement before the strain would have been provided. My approval of all requests was required.

I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under §1001 of title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the above application and any patent or application related thereto.

Gerald Fitzgerald

Gerald Fitzgerald

6th Oct 06

Date

Exhibit 1.

Curriculum Vitae

NAME: Gerald F. Fitzgerald
POSITION: Professor of Food Microbiology; Director, BioTransfer Unit, UCC

QUALIFICATIONS:

1978	BSc (Microbiology) University College Cork
1982	PhD (Microbiology) University College Cork
2006	DSc, National University of Ireland

BRIEF OUTLINE OF ACADEMIC HISTORY:

2004	Director, BioTransfer Unit, UCC
2003 – Present	Deputy Director, Alimentary Pharmabiotic Centre, UCC
2002- 2004	Head, Department of Microbiology
1999 – Present	Professor of Microbiology (Food Microbiology), UCC
1998 – 2004	Director, National Food Biotechnology Centre, UCC
1998 -1999	Associate Professor, Microbiology Department, UCC
1984 - 1998	Lecturer/Statutory Lecturer, Microbiology Department, UCC
1982-1984:	Postdoctoral Fellow, University of Michigan Dental School, Ann Arbor, MI, U.S.A.
1978 - 1982	PhD Graduate Student, University College Cork

RESEARCH INTERESTS

- Probiotic cultures - fundamental analysis and applications in foods
- Genomics of *Bifidobacterium*
- Molecular genetics of bacteriophage of *Lactococcus*
- Bacteriophage resistance in *Lactococcus* : fundamental analysis of resistance systems and their application in the construction of phage resistant cultures
- Biochemistry, physiology and genetics of Lactic Acid Bacteria
- Bacteriocins of Lactic Acid Bacteria as biopreservatives of foods

Total number of peer reviewed publications: 180+
Number of completed graduate student theses: 37 PhD; 24 MSc

Awards: Awarded Royal Irish Academy National Commission for Microbiology Medal for excellence in research (1995).
Career research funding generated: ¤7.5m from Enterprise Ireland, Department of Agriculture, Food and Rural Development, BioResearch Ireland, EU Commission, Industry, Health Research Board, Higher Education Authority.

Membership of editorial boards/scientific committees:
Editor for Applied and Environmental Microbiology for eight years;
Member of the Scientific Committee of the Food Safety Promotion Board
Member of the Novel Foods Committee of the Food Safety Authority of Ireland
External Examiner, Queen's University Belfast
Co-ordinator of several Department of Agriculture, Food and Rural Development and HEA research programmes; have previously co-ordinated large (50+ laboratories) EU projects

Exhibit 2.

ELSEVIER

FEMS Microbiology Letters 156 (1997) 259–264

FEMS MICROBIOLOGY LETTERS

Determination of genetic diversity within the genus *Bifidobacterium* and estimation of chromosomal size

Katie O'Riordan [a], Gerald F. Fitzgerald [a,b,*]

[a] *Department of Microbiology, University College, Cork, Ireland*
[b] *National Food Biotechnology Centre, University College, Cork, Ireland*

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Abstract

Pulsed-field gel electrophoresis was proven to be an efficient means of differentiating 25 strains of *Bifidobacterium* obtained from culture collections. *Xba*I, *Spe*I, *Dra*I restriction enzyme profiles indicated genomic heterogeneity among strains. When seven human isolates of bifidobacteria were compared using the same methods, two individual banding patterns were obtained. However, despite its discriminatory potential, pulsed-field gel electrophoresis was shown to be of no value in taxonomic identification. Genomic sizes estimated for eight *Bifidobacterium* strains ranged from 1.5 Mb to 2.1 Mb.

Keywords: *Bifidobacterium*; Pulsed-field gel electrophoresis; Chromosome size

1. Introduction

The genus *Bifidobacterium* is among the three most prevalent bacterial genera in the human colon. According to the most recent classification the genus consists of 32 species, 12 of which are of human origin [1]. Differentiation of species within this genus has traditionally relied on DNA-DNA homology or various phenotypic characteristics [2]. The reputed therapeutic value of these microorganisms has resulted in their incorporation into many functional foods. Because of this, considerable effort has since been devoted to the application of various molecular techniques for the rapid identification of strains. These include the use of genus-specific [3], species-specific [4] and strain-specific [5] probes based on appropriate 16S rRNA sequences. rRNA gene restriction patterns or randomly cloned DNA fragments as species-specific DNA probes have also been used to distinguish between species [6,7].

The technique of pulsed-field gel electrophoresis (PFGE) has been exploited to successfully unravel the organisation of many bacterial genomes revealing the presence of multiple chromosomes, linear chromosomes or large plasmids in different hosts. Rare cutting enzymes employed in conjunction with PFGE have allowed species identification and strain classification within the same species and have also provided useful data for estimating genome size and for genome mapping [8]. Until recently, information on genomic organisation of bifidobacteria was limited to one species of the genus which described intra-species polymorphisms between four of five *B.*

* Corresponding author. Tel.: +353 (21) 902730; Fax: +353 (21) 903101; E-mail: G.Fitzgerald@UCC.IE

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breve strains examined [9]. However, Roy et al. [10] provided a more extensive study, in which PFGE was used to compare a bank of dairy-related bifidobacteria comprising culture collection and commercial strains. The method was successful in distinguishing between strains even within a given species and in establishing the origin of commercial strains.

The aim of this study was to employ PFGE to (i) determine intra- and inter-species genetic diversity of a number of culture collection typed strains of bifidobacteria including representatives of the four prevalent human species, (ii) evaluate the technique of PFGE as a means of differentiating between and speciating a range of human bifidobacterial isolates, and (iii) estimate genomic sizes for representative strains.

2. Materials and methods

2.1. Bacterial strains

Bifidobacteria strains studied are listed in Table 1. Bifidobacteria were routinely cultured in TPY broth [11] at 37°C under anaerobic conditions which were maintained using the anaerobic Gas Pak system (Merck, Darmstadt, Germany) in an anaerobic chamber.

2.2. Preparation of bacterial plugs

Agarose plugs containing genomic DNA were prepared as follows: 100 ml volumes of TPY were inoculated (2%) with the appropriate microorganism. When an OD_{600nm} of ~ 1 was attained the cells were harvested, washed once in 50 mM EDTA, pH 8.5 and finally resuspended in 1.5 ml of the same solution. 500 μl of this cell suspension was heated to 42°C and mixed with 3 ml of molten 1% low melting point agarose and the resulting solution was poured into the mould chamber (Bio-Rad, Richmond, CA, USA). Solidified blocks were incubated for 4–16 h in lysozyme solution (2 mg ml^{-1} lysozyme, 0.05% *N*-lauryl sarcosine in 50 mM EDTA, pH 8.5). The blocks were then heated overnight (12–16 h) with proteinase K at 42°C (2 mg ml^{-1} proteinase K, 1% SDS. 0.1 M Tris in 50 mM EDTA, pH 8.5). Inserts were washed at least three times with 50 mM EDTA, pH 8.5 at room temperature with gentle shaking and were finally stored in the same solution at 4°C.

Table 1
Bifidobacterium strains

Species	Strain	Source
B. bifidum	NCFB 1452	Nursling stools
	NCFB 1453	Nursling stools
	NCFB 1454	Nursling stools
	NCFB 1455	Nursling stools
	NCFB 1456	Nursling stoold
	NCFB 2203	Infant intestine
	NCIMB 8810	Nursling stools
	Chr. Hansens 12	Commercial strain
B. infantis	NCFB 2255	Infant intestine
	NCFB 2256	Infant intestine
	NCFB 2205	Infant intestine
	Visby 420	Commercial strain
B. breve	NCFB 2257	Infant intestine
	NCFB 2258	Infant intestine
	NCIMB 8815	Nursling stools
	NCIMB 8807	Nursling stools
	NCTC 11815	Infant intestine
B. adolescentis	NCFB 2204	Adult intestine
	NCFB 2229	Adult intestine
	NCFB 2230	Adult intestine
	NCFB 2231	Adult intestine
	NCTC 11814	Adult intestine
Bifidobacterium sp.	UCC 35612	Adult intestine
	UCC 35624	Adult intestine
	UCC 35658	Adult intestine
	UCC 35652	Adult intestine
	UCC 35675	Adult intestine
	UCC 35678	Adult intestine
	UCC 35687	Adult intestine
B. angulatum	NCFB 2236	Human faeces
B. catenulatum	NCFB 2246	Human faeces
B. pseudocatenulatum	NCIMB 8811	Nursling stools

NCFB: National Collection of Food Bacteria, Reading, UK. NCIMB: National Collection of Industrial and Marine Bacteria, Aberdeen, UK. NCTC: National Culture Type Collection, London, UK. UCC: Culture Collection, University College, Cork, Ireland. Visby: Laboratorium Wiesby, Germany. Chr. Hansens Laboratory A/S, Copenhagen, Denmark.

2.3. Restriction digestion of DNA in agarose blocks

Agarose blocks were cut into 1×2×5 mm segments with a scalpel and washed in 1 ml sdH_2O on ice for 15 min to lower the EDTA concentration in the plug. The water was replaced with 100–200 μl restriction endonuclease buffer and left to equilibrate overnight at 4°C. The buffer was replaced and the

appropriate restriction endonuclease added. Digestion was performed at the recommended temperature for the chosen enzyme.

2.4. PFGE

Separation of DNA fragments was performed in a CHEF DR II apparatus (Bio-Rad). Agarose gels were prepared using 1% pulsed-field certified agarose (Bio-Rad) in 0.5×TBE (45 mM Tris, 45 mM boric acid, 1 mM EDTA, pH 8.0). Electrophoresis was performed at 8°C with pulse times varying with the size range of DNA fragments. To resolve fragments in the size range 150–600 kb switch times of 6–60 s were used, for 40–200 kb fragments switch times of 1–20 s, and for fragments of 20–45 kb switch times varied between 0.1 and 5 s. The sizes of the restriction fragments were determined by comparison with standard size markers. The standards used were Lambda ladder PFG Marker (48.5–1018.5 kb), Yeast Chromosome PFG Marker (225–1900 kb) and Low Range Marker (0.13–194 kb), all obtained from New England Biolabs (Beverly, MA). Gels were ethidium bromide-stained and photographed on a UV transilluminator using either a Polaroid MP4 Land camera containing type 667 film or a UVP image store 5000 Gel Documentation System linked to a Sony video graphic printer.

3. Results and discussion

Molecular technologies are currently the favoured methods for discriminating between strains of many different bacterial genera. In general, the available literature indicates that even though it is more time-consuming and labour-intensive, for many genera PFGE is more effective than ribotyping, SDS-PAGE or random amplified polymorphic DNA (RAPD) PCR assays in discriminating between strains [12]. Because of this PFGE was chosen in this study as a means of distinguishing between bifidobacterial strains. In this study 25 typed bifidobacterial strains representing the four predominant species present in the human intestine were first digested with restriction enzymes and resultant profiles compared. These included *B. bifidum* (8 strains), *B. adolescentis* (5 strains), *B. infantis* (4 strains), *B. breve* (5 strains) and three other strains (*B. angulatum*, *B. catenulatum*, *B. pseudocatenulatum*) of species less frequently isolated from humans. In addition seven human isolates were examined in a similar manner.

3.1. Selection of suitable enzymes for PFGE analysis of Bifidobacterium species

Physical genome analyses require restriction enzymes that cut the bacterial genome into a limited number of fragments. Due to the high GC content of bifidobacteria (55–64%) enzymes incorporating AT-rich sequence (*Dra*I, *Ase*I, *Ssp*I) or 8 bp sequence (*Sfi*I, *Not*I, *Pac*I, *Swa*I, *Ase*I) in their recognition sites or possessing the tetranucleotide CTAG in their restriction sites (*Xba*I, *Spe*I, *Avr*II) were tested, as these would be expected to cleave such genomes infrequently [13]. Only *Ase*I, *Spe*I and *Xba*I proved to be suitable in that they produced fewer than 30 bands. *Dra*I was a very effective rare cutter for *Bifidobacterium* sp. 35612 but continuously resulted in partial digests for a number of other strains. Employing different switch times enabled good resolution of fragments of all molecular masses.

3.2. Comparison of genomic restriction digest patterns of culture collection strains

It was of interest to study whether strains within the same species could be differentiated by PFGE. Initially the 25 culture collection strains were examined. These included some 'type' strains which, although obtained from different culture collections, are believed to be identical. Of the five *B. breve* strains analysed some appeared to be genetically similar (Fig. 1). The type strains 2257 and 11815 which are listed in the culture collections as being synonymous appeared indistinguishable when digested with *Xba*I (Fig. 1, lanes 1 and 5) and when digested with *Spe*I, profiles differed by only one band. Strains 8815 and 8807, which according to collection catalogues listings are phenotypically different, were shown to display very related patterns. *Xba*I macrorestriction analysis of these strains resulted in profiles with very minor differences (one obvious band; Fig. 1, lanes 3 and 4). When five strains of the species *B. adolescentis* were examined in a similar manner they also appeared genetically quite homologous, and

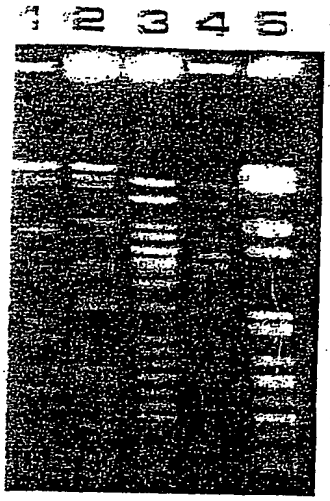

Fig. 1. *Xba*I macrorestriction profiles of five *B. breve* strains. PFGE was performed at 180 V for 24 h with a ramped switch time of 2–12 s. Lane 1, *B. breve* 2257; lane 2, *B. breve* 2258; lane 3, *B. breve* 8815; lane 4, *B. breve* 8807; lane 5, *B. breve* 11815.

again the type strains 11814 and 2204 produced the expected identical patterns when digested with *Xba*I, *Spe*I and *Dra*I (data not shown) reiterating the reproducibility of this method. The seven strains representing the species *B. bifidum* exhibited a greater degree of genomic heterogeneity with both *Xba*I and *Spe*I restriction digests (Fig. 2). The profiles obtained in this study for strain 2203 appeared to correlate well with *Xba*I/*Spe*I digests of the same strain (ATCC 15696) reported by Roy et al. [10]. The type strains 8810 and 1454 displayed identical patterns (data not shown) but in general the strains within this species appeared quite diverse. When strains of this and other species were compared, inter-species differences were not found to be any more pronounced than intra-species differences (Fig. 2). In fact, *B. pseudocatenulatum* 8811 and *B. bifidum* 1455 displayed identical patterns (Fig. 2, lanes 4 and 7). These strains, obtained from different culture collections, are believed to be phenotypically identical although speciated differently. While four strains from the species *B. infantis* were compared, all produced different patterns when digested with *Xba*I and *Spe*I (*Xba*I digests of three strains shown in Fig. 3, lanes 5, 6, 7). Intra-species relatedness did not appear to be greater than inter-species relatedness, e.g. when digested with the same enzyme, the

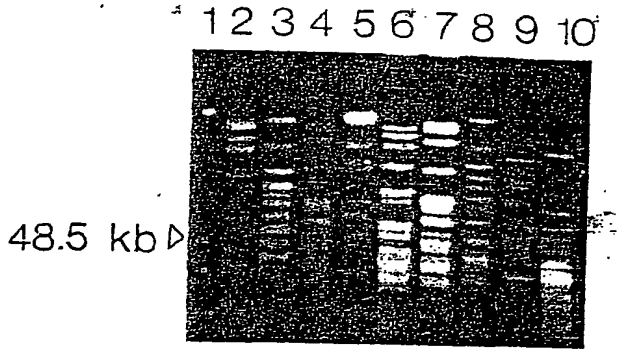

Fig. 2. Total DNA digested with *Spe*I. Gels were resolved at 180 V for 24 h with a ramped switch time of 2–12 s. Lane 1, low range PFG marker; lane 2, *B. bifidum* Chr. Hansens 12; lane 3, *B. catenulatum* 2236; lane 4, *B. pseudocatenulatum* 8811; lane 5, *B. bifidum* 2203; lane 6, *B. bifidum* 1456; lane 7, *B. bifidum* 1455; lane 8, *B. bifidum* 1454; lane 9, *B. bifidum* 1453; lane 10, *B. bifidum* 1452.

three largest *B. infantis* 2256 fragments co-migrated with three of the four largest *B. pseudocatenulatum* 8811 fragments, only one of which co-migrated with fragments from the related species *B. catenulatum* (Fig. 3, lanes 6, 3, 4). However, over a range of digests *B. catenulatum* and *B. pseudocatenulatum* were shown to consistently result in a greater number of co-migrating bands. DNA-DNA homology studies have indicated that the species *B. catenulatum* and *B. pseudocatenulatum* are very similar in that they exhibit degrees of homology as high as 75% [2]. In this study the similarity of macrorestriction

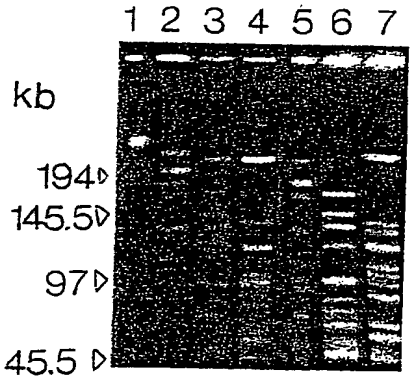

Fig. 3. *Xba*I digests of total DNA from *Bifidobacterium* strains. Gels were run at 180 V for 24 h with a ramped switch time of 2–10 s. Lane 1, low range PFG marker; lane 2, *B. angulatum* NCFB 2236; lane 3, *B. pseudocatenulatum* NCIMB 8811; lane 4, *B. catenulatum* NCFB 2246; lane 5, *B. infantis* Visby 420; lane 6, *B. infantis* NCFB 2256; lane 7, *B. infantis* NCFB 2255.

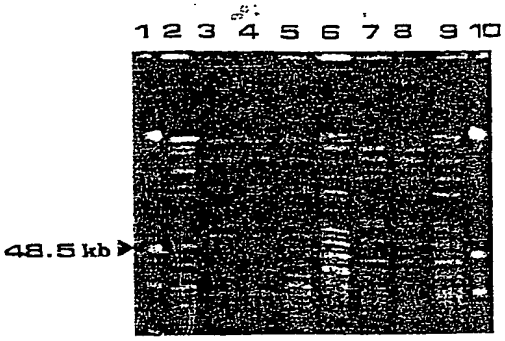

Fig. 4. Comparison of *Ase*I and *Asc*I digests of human bifidobacteria isolates. PFGE was performed at 180 V for 24 h with a ramped switch time of 3–5 s. Lane 1, low range PFG marker; lane 2, *B. bifidum* 2203 (*Ase*I); lane 3, *Bifidobacterium* isolate 35612 (*Ase*I); lane 4, *Bifidobacterium* isolate 35624 (*Ase*I); lane 5, *Bifidobacterium* isolate 35658 (*Ase*I); lane 6, *B. bifidum* 2203 (*Asc*I); lane 7, *Bifidobacterium* isolate 35612 (*Asc*I); lane 8, *Bifidobacterium* isolate 35624 (*Asc*I); lane 9, *Bifidobacterium* isolate 35658 (*Asc*I), lane 10, low range PFG marker.

patterns obtained for 1455 and 8811 with those obtained for *B. catenulatum* suggest that these strains are indeed better classified as *B. pseudocatenulatum*.

3.3. Comparison of genomic patterns of human isolates

A bank of seven human intestinal isolates, classified as members of the genus *Bifidobacterium* both by their 3:2 acetate:lactate ratio as determined by HPLC and by classical positive fructose 6-phosphate phosphoketolase reactions, were also compared by PFGE. As these particular strains were all isolated from one individual it was of interest to determine if they were identical. Therefore the strains were compared by restricting their genomic DNA with a number of enzymes (*Avr*II, *Dra*I, *Ase*I, *Xba*I, *Spe*I, *Not*I). Only two classes of restriction patterns were obtained with isolate 35658 displaying a different banding pattern to each of the other isolates. The two types of banding patterns generated for *Ase*I and *Asc*I are shown in Fig. 4 (lanes 3–5 and 7–9, respectively).

The patterns obtained from the two human isolate groups (represented by 35658 and 35612) were compared to digest patterns of a number of culture collection strains (*B. adolescentis, B. angulatum, B. bifidum; B. infantis, B. longum, B. pseudocatenulatum* and *B. breve*) in an attempt to identify the isolates to species level. However, although co-migrating bands could be identified, due to the extreme sensitivity of this method, species boundaries could not clearly be defined. It would therefore appear that although PFGE is a good discriminatory technique it would require a great deal of screening to establish its taxonomic relevance.

3.4. Genomic sizes

Genome sizes were estimated for eight strains representing different species (*Bifidobacterium* sp. 35612, *B. angulatum, B. catenulatum, B. pseudocatenulatum, B. bifidum, B. breve, B. infantis, B. adolescentis*; see Table 2). Fragments obtained from at least two different enzymes were sized. In addition, each gel was run under three different ramped switch times as described in Section 2 to obtain maximum resolution of different molecular mass fragments. In each case the size of the restriction fragments was determined as described by Heath et al. using two flanking size standards [14]. The presence of multiple bands was assessed by visual evaluation of ethidium bromide staining. Estimated genome sizes ranged from 1.5 Mb to 2.1 Mb with an average genome size of 1.8 Mb. This value places them in the lower category size range for bacterial chromosomes, smaller than

Table 2
Genome restriction analysis of *Bifidobacterium* strains by PFGE

Strain	Enzyme	Total number of restriction fragments	Genome size (Mb)
Bifidobacterium sp. 35612	*Xba*I	18	1.85
	*Spe*I	21	1.5
	*Dra*I	11	1.79
B. angulatum	*Xba*I	16	1.77
	*Spe*I	13	1.50
B. catenulatum	*Xba*I	18	1.46
	*Spe*I	18	1.69
B. pseudocatenulatum	*Xba*I	19	1.65
	*Spe*I	19	1.55
B. bifidum 8810	*Xba*I	16	1.96
	*Spe*I	25	1.80
B. breve 2257	*Xba*I	11	1.53
	*Spe*I	21	1.64
B. infantis 2255	*Xba*I	18	1.67
	*Spe*I	23	2.07
B. adolescentis 2231	*Xba*I	16	1.97
	*Spe*I	19	2.02

the genetically related Actinomycetaceae, *Streptomyces* sp. (6.5–8.2 Mb) and *Corynebacterium glutamicum* (2.987 Mb) [15]. PFGE although a popular method of chromosome sizing can at best only be relied on to give an estimated value. The values obtained for *B. breve* NCFB 2257 is very close to the 1.6 Mb value proposed by Roy et al. [10] for the synonymous strain *B. breve* ATCC 15700 but lower than the 2.1 Mb values reported by others for members of the same species [9]. Profiles obtained for *B. infantis* strain NCFB 2205, when compared to those described previously [10] for the equivalent strain ATCC 15697, revealed some slight differences. In this study a greater number of smaller sized bands resulted in a higher genomic size of approximately 1.87 Mb compared to the 1.5 Mb reported by Roy et al. [10]. This study is also the first to report estimated genome sizes for strains of *B. angulatum*, *B. catenulatum* or *B. pseudocatenulatum*.

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